

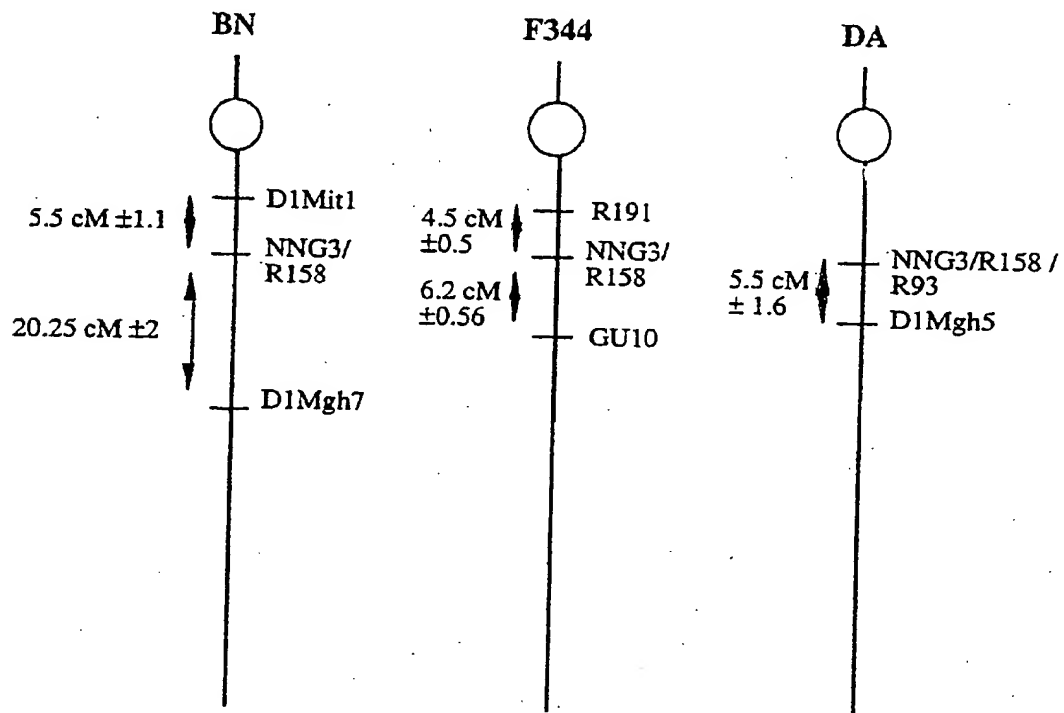
FIGURE 1

FIGURE 2

-140 -130 -120 -110 -100 -90

Contig
rat mRNA
113/114 NNG3
113/114 AS

TGCTTTCTGCCCTGCGCTGCGCACCGTTAGTGCCCTGCCCTGTCTTCCGATCTCAGAG
TGCTTTCTGCCCTGCGCTGCGCACCGTTAGTGCCCTGCCCTGTCTTCCGATCTCAGAG

-80 -70 -60 -50 -40 -30

Contig
rat mRNA
113/114 NNG3
113/114 AS

TCTGCGGAGTGCCCCCTATCGCCGTCCACCTGTTTCCTCAGAAAAAAGGCCAGCTCGTGAT
TCTGCGGAGTGCCCCCTATCGCCGTCCACCTGTTTCCTCAGAAAAAAGGCCAGCTCGTGAT

-20 -10 1 10 20 30

Contig
rat mRNA
113/114 NNG3
113/114 AS

CCCTGCTGCGTTCCTGGGGCCATGGCGGGTCTGGGTCTGGCGGGGGCGACTCAGAAGGG
CCCTGCTGCGTTCCTGGGGCCATGGCGGGTCTGGGTCTGGCGGGGGCGACTCAGAAGGG

Start Codon

40 50 60 70 80 90

Contig
rat mRNA
113/114 NNG3
113/114 AS

GGACCCCGACCCTGTTTTGCAGAAAGGGGGCGCTGAGGCAGAAGGTGGTCCACGAGGTG
GGACCCCGACCCTGTTTTGCAGAAAGGGGGCGCTGAGGCAGAAGGTGGTCCACGAGGTG

100 110 120 130 140 150

Contig
rat mRNA
113/114 NNG3
113/114 AS

AAGAGCCACAAGTTCACCGCTCGTTTCTTCAAGCAGCCAACCTTCTGCAGTCACTGTACC
AAGAGCCACAAGTTCACCGCTCGTTTCTTCAAGCAGCCAACCTTCTGCAGTCACTGTACC

160 170 180 190 200 210

Contig
rat mRNA
113/114 NNG3
113/114 AS

GACTTCATCTGGGGCATTTGGAAAGCAGGGCCTGCAATGTCAAGTCTGCAGCTTTGTGGTT
GACTTCATCTGGGGCATTTGGAAAGCAGGGCCTGCAATGTCAAGTCTGCAGCTTTGTGGTT

220 230 240 250 260 270

Contig
rat mRNA
113/114 NNG3
113/114 AS

CACCGCCGATGCCACGAATTGTGACCTTCGAGTGTCCAGGCGCTGGAAGGGCCCCCAG
CACCGCCGATGCCACGAATTGTGACCTTCGAGTGTCCAGGCGCTGGAAGGGCCCCCAG

280 290 300 310 320 330

Contig
rat mRNA
113/114 NNG3
113/114 AS

ACGGACGACCCTCGCAACAAGCACAAGTTCGGTCTGCACAGCTACAGCAGTCCCACCTTC
ACGGACGACCCTCGCAACAAGCACAAGTTCGGTCTGCACAGCTACAGCAGTCCCACCTTC

340 350 360 370 380 390

Contig
rat mRNA
113/114 NNG3
113/114 AS

TGCGACCACTGTGGTTCCCTCCTCTACGGGCTGGTGCACCAGGGCATGAAATGTTCTCTGT
TGCGACCACTGTGGTTCCCTCCTCTACGGGCTGGTGCACCAGGGCATGAAATGTTCTCTGT

400 410 420 430 440 450

Contig
rat mRNA
113/114 NNG3
113/114 AS

TGCGAAATGAATGTGCACCGACGCTGTGTGCGCAGCGTGCCCTCCCTTTGCGGCGTGGAC
TGCGAAATGAATGTGCACCGACGCTGTGTGCGCAGCGTGCCCTCCCTTTGCGGCGTGGAC

460 470 480 490 500 510

Contig
rat mRNA
113/114 NNG3
113/114 AS

CATACAGAGCGCCGTGGACGTCTGCAACTGGAAATCCGGGCTCCACATCAGATGAGATC
CATACAGAGCGCCGTGGACGTCTGCAACTGGAAATCCGGGCTCCACATCAGATGAGATC

3/26

FIGURE 2 (CONT)

520 530 540 550 560 570
| | | | | |
Contig CATATTACTGTGGGTGAGGCCCGGAACCTCATTCTATGGACCCCAATGGCCTGTCTGAT
rat mRNA CATATTACTGTGGGTGAGGCCCGGAACCTCATTCTATGGACCCCAATGGCCTGTCTGAT
113/114 NNG3
113/114 AS Proof

580 590 600 610 620 630
| | | | | |
Contig CCCTATGTGAAACTGAAGCTCATCCCGGACCCTCGGAACCTGACAAAACAGAAGACAAAG
rat mRNA CCCTATGTGAAACTGAAGCTCATCCCGGACCCTCGGAACCTGACAAAACAGAAGACAAAG
113/114 NNG3
113/114 AS

640 650 660 670 680 690
| | | | | |
Contig ACCGTGAAAGCCACACTGAATCCCGTGTGGAACGAGACCTTCGTGTTCAACCTGAAGCCG
rat mRNA ACCGTGAAAGCCACACTGAATCCCGTGTGGAACGAGACCTTCGTGTTCAACCTGAAGCCG
113/114 NNG3
113/114 AS

700 710 720 730 740 750
| | | | | |
Contig GGGGATGTGGAGCGCCGGCTCAGTGTGGAGGTGTGGGATTGGGATAGGACATCCCGAAAT
rat mRNA GGGGATGTGGAGCGCCGGCTCAGTGTGGAGGTGTGGGATTGGGATAGGACATCCCGAAAT
113/114 NNG3
113/114 AS

760 770 780 790 800 810
| | | | | |
Contig GACTTCATGGGTGCCATGTCCTTTGGTGTCTCAGAGCTACTCAAGGCTCCTGTGGATGGA
rat mRNA GACTTCATGGGTGCCATGTCCTTTGGTGTCTCAGAGCTACTCAAGGCTCCTGTGGATGGA
113/114 NNG3
113/114 AS

820 830 840 850 860 870
| | | | | |
Contig TGGTACAAGTTACTGAACCAGKAGGAGGGCGAGTATTACAATGTACCGGTGGCCGATGC
rat mRNA TGGTACAAGTTACTGAACCAGGAGGAGGGCGAGTATTACAATGTACCGGTGGCCGATGC
113/114 NNG3
113/114 AS
ACAAGTTACTGAACCAGUAGGAGGGCGAGTATTACAATGTACCGGTGGCCGATGC
ACAAGTTACTGAACCAGGAGGAGGGCGAGTATTACAATGTACCGGTGGCCGATGC

880 890 900 910 920 930
| | | | | |
Contig TGACAACTGCAGCCTCCTCCAGAAGTTTGAGGCCTGTAATTACCCCTTGAATTGTATGA
rat mRNA TGACAACTGCAGCCTCCTCCAGAAGTTTGAGGCCTGTAATTACCCCTTGAATTGTATGA
113/114 NNG3
113/114 AS
TGACAACTGCAGCCTCCTCCAGAAGTTTGAGGCCTGTAATTACCCCTTGAATTGTATGA
TGACAACTGCAGCCTCCTCCAGAAGTTTGAGGCCTGTAATTACCCCTTGAATTGTATGA

940 950 960 970 980 990
| | | | | |
Contig GAGAGTGCAGGATGGGCCCCCTTCTCTCTCCATTCTCTCTCCATCCCCCAGTCCCACGGA
rat mRNA GAGAGTGCAGGATGGGCCCCCTTCTCTCTCCATTCTCTCTCCATCCCCCAGTCCCACGGA
113/114 NNG3
113/114 AS
GAGAGTGCAGGATGGGCCCCCTTCTCTCTCCATTCTCTCTCCATCCCCCAGTCCCACGGA
GAGAGTGCAGGATGGGCCCCCTTCTCTCTCCATTCTCTCTCCATCCCCCAGTCCCACGGA

1000 1010 1020 1030 1040 1050
| | | | | |
Contig CTCCAAGAGATGCTTCTTCGGTGCCAGCCAGGACGCCTGCATATCTCTGACTTCAGCTT
rat mRNA CTCCAAGAGATGCTTCTTCGGTGCCAGCCAGGACGCCTGCATATCTCTGACTTCAGCTT
113/114 NNG3
113/114 AS
CTCCAAGAGATGCTTCTTCGGTGCCAGCCAGGACGCCTGCATATCTCTGACTTCAGCTT
CTCCAAGAGATGCTTCTTCGGTGCCAGCCAGGACGCCTGCATATCTCTGACTTCAGCTT

1060 1070 1080 1090 1100 1110
| | | | | |
Contig CCTCATGGTTCTAGGGAAAGGCAGTTTTGGGAAGGTGATGCTGGCAGARCGCAGAGGATC
rat mRNA CCTCATGGTTCTAGGGAAAGGCAGTTTTGGGAAGGTGATGCTGGCAGAGCGCAGAGGATC
113/114 NNG3
113/114 AS
CCTCATGGTTCTAGGGAAAGGCAGTTTTGGGAAGGTGATGCTGGCAGAGCGCAGAGGATC
CCTCATGGTTCTAGGGAAAGGCAGTTTTGGGAAGGTGATGCTGGCAGAACGCAGAGGATC

FIGURE 2 (CONT)

1120 1130 1140 1150 1160 1170
| | | | | |
Contig CGATGAACCTCTATGCCATCAAGATNCTGAAAAAAGACGTCATTGTCCAGGATGATGATGT
rat mRNA CGATGAACCTCTATGCCATCAAGATACTGAAAAAAGACGTCATTGTCCAGGATGATGATGT
113/114 NNG3 CGATGAACCTCTATGCCATCAAGATACTGAAAAA
113/114 AS CGATGAACCTCTATGCCATCAAGATNCTGAAAAA

1180 1190 1200 1210 1220 1230
| | | | | |
Contig AGACTGCACCCTTGTGGAGAAGCGTGTGCTGGCATTGGGAGGCCGAGGTCCTGGAGGCCG
rat mRNA AGACTGCACCCTTGTGGAGAAGCGTGTGCTGGCATTGGGAGGCCGAGGTCCTGGAGGCCG
113/114 NNG3
113/114 AS

1240 1250 1260 1270 1280 1290
| | | | | |
Contig GCCACACTTCTCACACAACCTTCATTCCACCTTTCAGACTCCGGACCGCCTGTATTTTGT
rat mRNA GCCACACTTCTCACACAACCTTCATTCCACCTTTCAGACTCCGGACCGCCTGTATTTTGT
113/114 NNG3
113/114 AS

1300 1310 1320 1330 1340 1350
| | | | | |
Contig GATGGAGTACGTCACCTGCGGGCGATTTAATGTACCACATTGAGCAACTGGGCAAGTTTAA
rat mRNA GATGGAGTACGTCACCTGCGGGCGATTTAATGTACCACATTGAGCAACTGGGCAAGTTTAA
113/114 NNG3
113/114 AS

1360 1370 1380 1390 1400 1410
| | | | | |
Contig GGAGCCCCACGCAGCATTCTATGCCGCGGAAATCGCCATAGGCCTCTTCTTCTTCACAA
rat mRNA GGAGCCCCACGCAGCATTCTATGCCGCGGAAATCGCCATAGGCCTCTTCTTCTTCACAA
113/114 NNG3
113/114 AS

1420 1430 1440 1450 1460 1470
| | | | | |
Contig CCAGGGCATCATCTACAGGGACCTCAAGTTGGATAATGTGATGCTGGATGCTGAAGGACA
rat mRNA CCAGGGCATCATCTACAGGGACCTCAAGTTGGATAATGTGATGCTGGATGCTGAAGGACA
113/114 NNG3
113/114 AS

1480 1490 1500 1510 1520 1530
| | | | | |
Contig CATCAAGATCACAGACTTCGGCATGTGTAAAGAGAATGTCTTCCCTGGGTCCACAACCCG
rat mRNA CATCAAGATCACAGACTTCGGCATGTGTAAAGAGAATGTCTTCCCTGGGTCCACAACCCG
113/114 NNG3
113/114 AS

1540 1550 1560 1570 1580 1590
| | | | | |
Contig CACCTTCTGTGGGACCCAGACTACATAGCACCTGAGATCATTGCCTATCAGCCCTATGG
rat mRNA CACCTTCTGTGGGACCCAGACTACATAGCACCTGAGATCATTGCCTATCAGCCCTATGG
113/114 NNG3
113/114 AS

1600 1610 1620 1630 1640 1650
| | | | | |
Contig GAAGTCTGTCGACTGGTGGTCTTTGGAGTCTGCTGTATGAGATGTTGGCAGGACAGCC
rat mRNA GAAGTCTGTCGACTGGTGGTCTTTGGAGTCTGCTGTATGAGATGTTGGCAGGACAGCC
113/114 NNG3
113/114 AS

1660 1670 1680 1690 1700 1710
| | | | | |
Contig ACCCTTTGATGGGGAAGATGAGGAGGAGCTGTTTCAAGCCATCATGGAACAACTGTCAC
rat mRNA ACCCTTTGATGGGGAAGATGAGGAGGAGCTGTTTCAAGCCATCATGGAACAACTGTCAC
113/114 NNG3
113/114 AS

1720 1730 1740 1750 1760 1770
| | | | | |
Contig CTATCCCAAGTCACTTTCCCGGGAAGCTGTGGCCATCTGCAAGGGGTTCTTGACCAAGCA
rat mRNA CTATCCCAAGTCACTTTCCCGGGAAGCTGTGGCCATCTGCAAGGGGTTCTTGACCAAGCA
113/114 NNG3
113/114 AS

5/26

FIGURE 2 (CONT)

1780 1790 1800 1810 1820 1830
Contig
rat mRNA
113/114 NNG3
113/114 AS
CCCAGGAAAGCGCCTGGGCTCAGGGCCAGATGGGGAACCCACCATCCGGGGCTCATGGCTT
CCCAGGAAAGCGCCTGGGCTCAGGGCCAGATGGGGAACCCACCATCCGGGGCTCATGGCTT

1840 1850 1860 1870 1880 1890
Contig
rat mRNA
113/114 NNG3
113/114 AS
TTTCCGTTGGATCGATTGGGAGAGGTTGGAGAGACTGGAAATTGCGCCTCCTTTTAGACC
TTTCCGTTGGATCGATTGGGAGAGGTTGGAGAGACTGGAAATTGCGCCTCCTTTTAGACC

1900 1910 1920 1930 1940 1950
Contig
rat mRNA
113/114 NNG3
113/114 AS
ACGTCCGTGTGGCCGAGCGGCGGAAACTTTGACAAGTTCTTCACGCGGGCAGCGCCAGC
ACGTCCGTGTGGCCGAGCGGCGGAAACTTTGACAAGTTCTTCACGCGGGCAGCGCCAGC

1960 1970 1980 1990 2000 2010
Contig
rat mRNA
113/114 NNG3
113/114 AS
CTTGACCCCGCCAGACCGCTTGGTCTAGCCAGCATCGACCAAGCTGATTTCCAGGGCTT
CTTGACCCCGCCAGACCGCTTGGTCTAGCCAGCATCGACCAAGCTGATTTCCAGGGCTT

2020 2030 2040 2050 2060 2070
Contig
rat mRNA
113/114 NNG3
113/114 AS
TACTTATGTGAACCCGGAATTCGTGCACCCAGATGCCCCGAGCCCCACAAGCCCTGTGCC
TACTTATGTGAACCCGGAATTCGTGCACCCAGATGCCCCGAGCCCCACAAGCCCTGTGCC

2080 2090 2100 2110 2120 2130
Contig
rat mRNA
113/114 NNG3
113/114 AS
TGTGCCCCGTCAATGTAATCTCATCTGCTGCCGCTAGGTGTTCCCAAGTCTCCCTCCGCCAA
TGTGCCCCGTCAATGTAATCTCATCTGCTGCCGCTAGGTGTTCCCAAGTCTCCCTCCGCCAA
Stop Codon

2140 2150 2160 2170 2180 2190
Contig
rat mRNA
113/114 NNG3
113/114 AS
GTTGGCTGTAACCTCCCATCCACCCCATCCCCGCCTCTAGTCCGAATTTTAGGTCTCTTA
GTTGGCTGTAACCTCCCATCCACCCCATCCCCGCCTCTAGTCCGAATTTTAGGTCTCTTA

2200 2210 2220 2230 2240 2250
Contig
rat mRNA
113/114 NNG3
113/114 AS
AACCACCCAACCTTCTGGCCTCTTTCACGCGCCCCAAGTGGGTTCTAGACGCTGTTCCCC
AACCACCCAACCTTCTGGCCTCTTTCACGCGCCCCAAGTGGGTTCTAGACGCTGTTCCCC

2260 2270 2280 2290 2300 2310
Contig
rat mRNA
113/114 NNG3
113/114 AS
AGCATTGCTGGCATTTTAAACTTCAAACAGTCTCTAGAGCCTTTCTGTGTTCTAGATTCTG
AGCATTGCTGGCATTTTAAACTTCAAACAGTCTCTAGAGCCTTTCTGTGTTCTAGATTCTG

2320 2330 2340 2350 2360 2370
Contig
rat mRNA
113/114 NNG3
113/114 AS
TTGTGCTGAGCCCTGGTTTTTCCCCACCCCCAACATCTGGATGCTGTTCCAACCTCTTCCC
TTGTGCTGAGCCCTGGTTTTTCCCCACCCCCAACATCTGGATGCTGTTCCAACCTCTTCCC

2380 2390 2400 2410 2420 2430
Contig
rat mRNA
113/114 NNG3
113/114 AS
AGAAACCCCACTCCGTGTGGGGTTCTAGACTCTATCTTGGTAGTTTTATGCCTTCTCTCT
AGAAACCCCACTCCGTGTGGGGTTCTAGACTCTATCTTGGTAGTTTTATGCCTTCTCTCT

7/26

FIGURE 3

-141
 -134 TGCCCTGCGCTGCGCACCGTTAGTGCCCTGCCCTGTCTCCGATCTCAGAGTCTGCGGAGTGCCC
 -67 CTATCGCCGTCCACCTGTTTCTCTCAGAAAAAGGCCAGCTCGTGATCCCTGCTGCGTTCCTGGGGCC

Start Ala Gly Leu Gly Pro Gly Gly Gly Asp Ser Glu Gly Gly Pro Arg Pro 17
 1 ATG GCG GGT CTG GGT CCT GGC GGG GGC GAC TCA GAA GGG GGA CCC CGA CCC

Leu Phe Cys Arg Lys Gly Ala Leu Arg Gln Lys Val Val His Glu Val Lys 34
 52 CTG TTT TGC AGA AAG GGG GCG CTG AGG CAG AAG GTG GTC CAC GAG GTG AAG

Ser His Lys Phe Thr Ala Arg Phe Phe Lys Gln Pro Thr Phe Cys Ser His 51
 103 AGC CAC AAG TTC ACC GCT CGT TTC TTC AAG CAG CCA ACC TTC TGC AGT CAC

Cys Thr Asp Phe Ile Trp Gly Ile Gly Lys Gln Gly Leu Gln Cys Gln Val 68
 154 TGT ACC GAC TTC ATC TGG GGC ATT GGA AAG CAG GGC CTG CAA TGT CAA GTC

Cys Ser Phe Val Val His Arg Arg Cys His Glu Phe Val Thr Phe Glu Cys 85
 205 TGC AGC TTT GTG GTT CAC CGC CGA TGC CAC GAA TTT GTG ACC TTC GAG TGT

Pro Gly Ala Gly Lys Gly Pro Gln Thr Asp Asp Pro Arg Asn Lys His Lys 102
 256 CCA GGC GCT GGA AAG GGC CCC CAG ACG GAC GAC CCT CGC AAC AAG CAC AAG

Phe Arg Leu His Ser Tyr Ser Ser Pro Thr Phe Cys Asp His Cys Gly Ser 119
 307 TTC CGT CTG CAC AGC TAC AGC AGT CCC ACC TTC TGC GAC CAC TGT GGT TCC

Leu Leu Tyr Gly Leu Val His Gln Gly Met Lys Cys Ser Cys Cys Glu Met 136
 358 CTC CTC TAC GGG CTG GTG CAC CAG GGC ATG AAA TGT TCC TGT TGC GAA ATG

Asn Val His Arg Arg Cys Val Arg Ser Val Pro Ser Leu Cys Gly Val Asp 153
 409 AAT GTG CAC CGA CGC TGT GTG CGC AGC GTG CCC TCC CTT TGC GGC GTG GAC

His Thr Glu Arg Arg Gly Arg Leu Gln Leu Glu Ile Arg Ala Pro Thr Ser 170
 460 CAT ACA GAG CGC CGT GGA CGT CTG CAA CTG GAA ATC CGG GCT CCC ACA TCA

Asp Glu Ile His Ile Thr Val Gly Glu Ala Arg Asn Leu Ile Pro Met Asp 187
 511 GAT GAG ATC CAT ATT ACT GTG GGT GAG GCC CGG AAC CTC ATT CCT ATG GAC

Pro Asn Gly Leu Ser Asp Pro Tyr Val Lys Leu Lys Leu Ile Pro Asp Pro 204
 562 CCC AAT GGC CTG TCT GAT CCC TAT GTG AAA CTG AAG CTC ATC CCG GAC CCT

Arg Asn Leu Thr Lys Gln Lys Thr Lys Thr Val Lys Ala Thr Leu Asn Pro 221
 613 CGG AAC CTG ACA AAA CAG AAG ACA AAG ACC GTG AAA GCC ACA CTG AAT CCC

Val Trp Asn Glu Thr Phe Val Phe Asn Leu Lys Pro Gly Asp Val Glu Arg 238
 664 GTG TGG AAC GAG ACC TTC GTG TTC AAC CTG AAG CCG GGG GAT GTG GAG CGC

Arg Leu Ser Val Glu Val Trp Asp Trp Asp Arg Thr Ser Arg Asn Asp Phe 255
 715 CGG CTC AGT GTG GAG GTG TGG GAT TGG GAT AGG ACA TCC CGA AAT GAC TTC

Met Gly Ala Met Ser Phe Gly Val Ser Glu Leu Leu Lys Ala Pro Val Asp 272
 766 ATG GGT GCC ATG TCC TTT GGT GTC TCA GAG CTA CTC AAG GCT CCT GTG GAT

Gly Trp Tyr Lys Leu Leu Asn Gln Glu Glu Gly Glu Tyr Tyr Asn Val Pro 289
 817 GGA TGG TAC AAG TTA CTG AAC CAG GAG GAG GGC GAG TAT TAC AAT GTA CCG
 TAG

Mutant NNG3 STOP

Val Ala Asp Ala Asp Asn Cys Ser Leu Leu Gln Lys Phe Glu Ala Cys Asn 306
 868 GTG GCC GAT GCT GAC AAC TGC AGC CTC CTC CAG AAG TTT GAG GCC TGT AAT

Tyr Pro Leu Glu Leu Tyr Glu Arg Val Arg Met Gly Pro Ser Ser Ser Pro 323
 919 TAC CCC TTG GAA TTG TAT GAG AGA GTG CGG ATG GGC CCC TCT TCC TCT CCC

Ile Pro Ser Pro Ser Pro Ser Pro Thr Asp Ser Lys Arg Cys Phe Phe Gly 340
 970 ATT CCT TCT CCA TCC CCC AGT CCC ACG GAC TCC AAG AGA TGC TTC TTC GGT

8/26

FIGURE 3 (CONT)

1021 Ala Ser Pro Gly Arg Leu His Ile Ser Asp Phe Ser Phe Leu Met Val Leu 357
 GCC AGC CCA GGA CGC CTG CAT ATC TCT GAC TTC AGC TTC CTC ATG GTT CTA
 1072 Gly Lys Gly Ser Phe Gly Lys Val Met Leu Ala Glu Arg Arg Gly Ser Asp 374
 GGG AAA GGC AGT TTT GGG AAG GTG ATG CTG GCA GAG CGC AGA GGA TCC GAT
 1123 Glu Leu Tyr Ala Ile Lys Ile Leu Lys Lys Asp Val Ile Val Gln Asp Asp 391
 GAA CTC TAT GCC ATC AAG ATA CTG AAA AAA GAC GTC ATT GTC CAG GAT GAT
 1174 Asp Val Asp Cys Thr Leu Val Glu Lys Arg Val Leu Ala Leu Gly Gly Arg 408
 GAT GTA GAC TGC ACC CTT GTG GAG AAG CGT GTG CTG GCA TTG GGA GGC CGA
 1225 Gly Pro Gly Gly Arg Pro His Phe Leu Thr Gln Leu His Ser Thr Phe Gln 425
 GGT CCT GGA GGC CGG CCA CAC TTT CTC ACA CAA CTT CAT TCC ACC TTT CAG
 1276 Thr Pro Asp Arg Leu Tyr Phe Val Met Glu Tyr Val Thr Gly Gly Asp Leu 442
 ACT CCG GAC CGC CTG TAT TTT GTG ATG GAG TAC GTC ACT GGG GGC GAT TTA
 1327 Met Tyr His Ile Gln Gln Leu Gly Lys Phe Lys Glu Pro His Ala Ala Phe 459
 ATG TAC CAC ATT CAG CAA CTG GGC AAG TTT AAG GAG CCC CAC GCA GCA TTC
 1378 Tyr Ala Ala Glu Ile Ala Ile Gly Leu Phe Phe Leu His Asn Gln Gly Ile 476
 TAT GCC GCG GAA ATC GCC ATA GGC CTC TTC TTC CTT CAC AAC CAG GGC ATC
 1429 Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Met Leu Asp Ala Glu Gly His 493
 ATC TAC AGG GAC CTC AAG TTG GAT AAT GTG ATG CTG GAT GCT GAA GGA CAC
 1480 Ile Lys Ile Thr Asp Phe Gly Met Cys Lys Glu Asn Val Phe Pro Gly Ser 510
 ATC AAG ATC ACA GAC TTC GGC ATG TGT AAA GAG AAT GTC TTC CCT GGG TCC
 1531 Thr Thr Arg Thr Phe Cys Gly Thr Pro Asp Tyr Ile Ala Pro Glu Ile Ile 527
 ACA ACC CGC ACC TTC TGT GGG ACC CCA GAC TAC ATA GCA CCT GAG ATC ATT
 1582 Ala Tyr Gln Pro Tyr Gly Lys Ser Val Asp Trp Trp Ser Phe Gly Val Leu 544
 GCC TAT CAG CCC TAT GGG AAG TCT GTC GAC TGG TGG TCC TTT GGA GTC CTG
 1633 Leu Tyr Glu Met Leu Ala Gly Gln Pro Pro Phe Asp Gly Glu Asp Glu Glu 561
 CTG TAT GAG ATG TTG GCA GGA CAG CCA CCC TTT GAT GGG GAA GAT GAG GAG
 1684 Glu Leu Phe Gln Ala Ile Met Glu Gln Thr Val Thr Tyr Pro Lys Ser Leu 578
 GAG CTG TTT CAA GCC ATC ATG GAA CAA ACT GTC ACC TAT CCC AAG TCA CTT
 1735 Ser Arg Glu Ala Val Ala Ile Cys Lys Gly Phe Leu Thr Lys His Pro Gly 595
 TCC CGG GAA GCT GTG GCC ATC TGC AAG GGG TTC CTG ACC AAG CAC CCA GGA
 1786 Lys Arg Leu Gly Ser Gly Pro Asp Gly Glu Pro Thr Ile Arg Ala His Gly 612
 AAG CGC CTG GGC TCA GGG CCA GAT GGG GAA CCC ACC ATC CGG GCT CAT GGC
 1837 Phe Phe Arg Trp Ile Asp Trp Glu Arg Leu Glu Arg Leu Glu Ile Ala Pro 629
 TTT TTC CGT TGG ATC GAT TGG GAG AGG TTG GAG AGA CTG GAA ATT GCG CCT
 1888 Pro Phe Arg Pro Arg Pro Cys Gly Arg Ser Gly Glu Asn Phe Asp Lys Phe 646
 CCT TTT AGA CCA CGT CCG TGT GGC CGC AGC GGC GAA AAC TTT GAC AAG TTC
 1939 Phe Thr Arg Ala Ala Pro Ala Leu Thr Pro Pro Asp Arg Leu Val Leu Ala 663
 TTC ACG CGG GCA GCG CCA GCC TTG ACC CCG CCA GAC CGC TTG GTC CTA GCC
 1990 Ser Ile Asp Gln Ala Asp Phe Gln Gly Phe Thr Tyr Val Asn Pro Asp Phe 680
 AGC ATC GAC CAA GCT GAT TTC CAG GGC TTT ACT TAT GTG AAC CCG GAC TTC
 2014 Val His Pro Asp Ala Arg Ser Pro Thr Ser Pro Val Pro Val Pro Val Met 697
 GTG CAC CCA GAT GCC CGC AGC CCC ACA AGC CCT GTG CCT GTG CCC GTC ATG

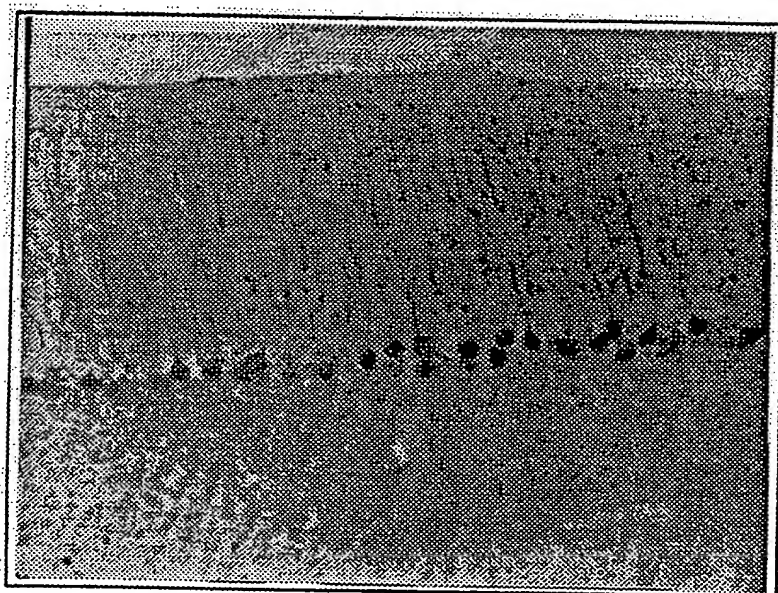
9/26

FIGURE 3 (CONT)

Stop

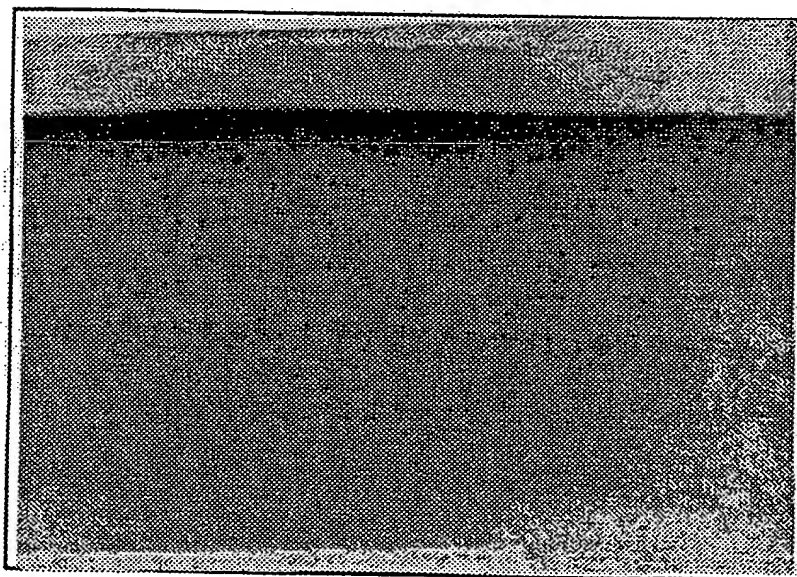
2092 TAA TCTCATCTGCTGCCGCTAGGTGTTCCAGTGCTCCCTCCGCCAAGTTGGCTGTAACTCCCATC
2158 CACCCCATCCCCGCTCTAGTCCGAATTTAGGTCTCTTAAACCACCCAACCTTCTGGCCTCTTTC
2225 ACGCGCCCCAAGTGGGTCTAGACGCTGTCCCCAGCATTGCTGGCATTTTAAACTTCAAACAGTCT
2292 CTAGAGCCTTTCTGTGTTCTAGATTGCTGTGCTGAGCCCTGGTTTTTCCCCACCCCCAACATCTGG
2359 ATGCTGTTCCAACCTCTTCCCAGAAACCCCACTCCGTGTGGGGTCTAGACTCTATCTTGGTAGTTTT
2426 ATGCCTTCTCTCCTTAGACCACGTTGGGAGAAATAGTCTCATGAGATTGCCTGCTCCAGACTAAG
2493 ATTCCAGATCAGCTCTCTGCATCCTTCAAGGCCCTCCTACCTCCACTTCAGTTGTAGAATTAAGTG
2560 GGAGGCTGGGCTCCGTGTTCCAGGCCACCTCCCTTCCATGTTCTGGGGATTCTGGCATGCACGGAG
2627 GATTCTCTCCCCGACTTTTCTCAGTCAGCTTTTGTCTAGATTGTTCCAGAACCCTTCACTGCTCA
2694 CCTGCCCCGTGCATGGCTCCAGCCTTGGTCGGAATCACACACACACACACACACACACACACACA
2761 CACACACACACACACACACACACACACCCCTTGTCTCCGCACTGCTGCCACTTTCTGGGACTTTCTCATCC
2828 CCCACGCCCTTCCTTTATCCTCTCCACCCAGACACAGCTGCTGGAGAATAAATTG

10/26

FIGURE 4**A**

← Granule cell
layer

← Purkinje cell
layer

B

← Granule cell
layer

← Purkinje cell
layer

11/26

FIGURE 5

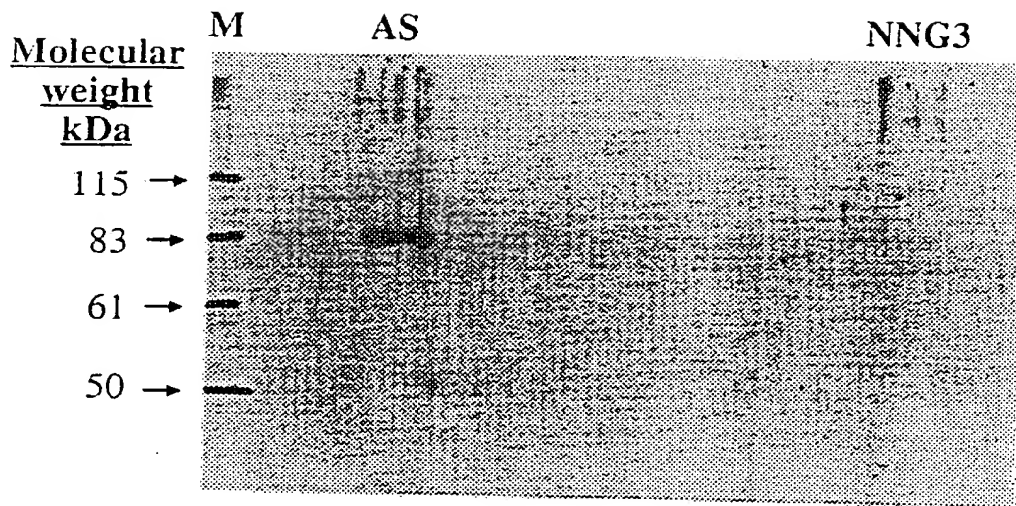
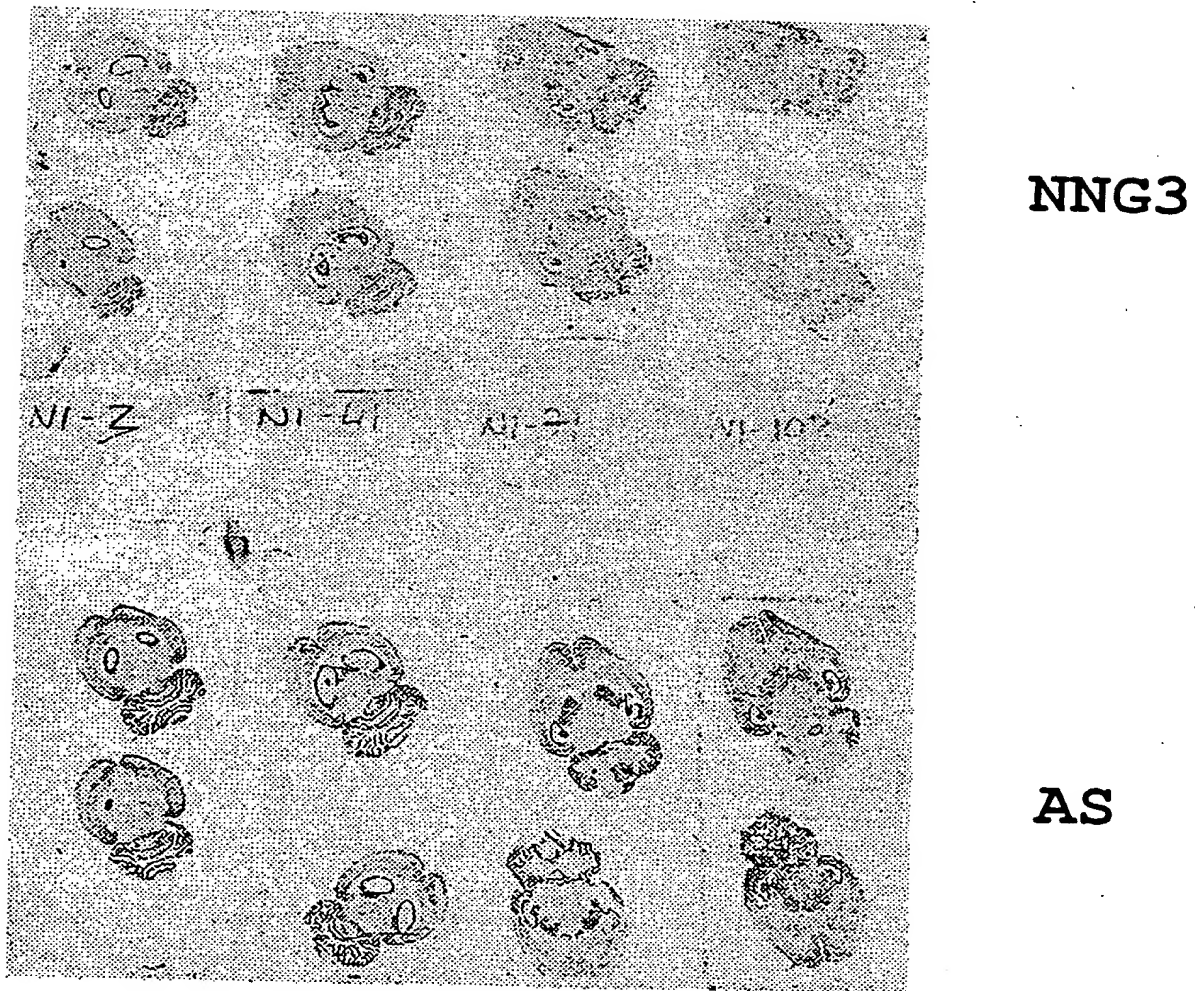


FIGURE 6



12/26

FIGURE 7

-140 -130 -120 -110 -100 -90 -80 -70
TGCTTTCTGCCCTGCGCTGCGCACCGTTAGTGCCCTGCCCTGTCCTTCCGATCTCAGAGTCTGCGGAGTGCCCTTA
.....
TCCTTCCGATCTCAGAGTCTGCGGAGTGCCCTTA

-60 -50 -40 -30 -20 -10 1 10
TCGCCGTCCACCTGTTTCCTCAGAAAAAGGCCAGCTCGTGATCCCTGCTGCGTTCTTGGGGCCATGGCGGGTCTGG
.....
TCGCCGTCCACCTGTTTCCTCAGAAAAAGGCCAGCTCGTGATCCCTGCTGCGTTCTTGGGGCCATGGCGGGTCTGG

Start codon

20 30 40 50 60 70 80 90
GTCCTGGCGGGGCGACTCAGAAGGGGGACCCGACCCCTGTTTTCAGAAAGGGGGCGCTGAGGCAGAAGGTGGTC
.....
GTCCTGGCGGGGCGACTCAGAAGGGGGACCCGACCCCTGTTTTCAGAAAGGGGGCGCTGAGGCAGAAGGTGGTC

100 110 120 130 140 150 160
CACGAGGTGAAGAGCCACAAGTTCACCGCTCGTTTCTTCAAGCAGCCAACCTTCTGCAGTCACTGTACCGACTTCAT
.....
CACGAGGTGAAGAGCCACAAGTTCACCGCTCGTTTCTTCAAGCAGCCAACCTTCTGCAGTCACTGTACCGACTTCAT

170 180 190 200 210 220 230 240
CTGGGGCATTGGAAGCAGGGCCTGCAATGTCAAGTCTGCAGCTTTGTGGTTCACCGCCGATGCCACGAATTTGTGA
.....
CTGGGGCATTGGAAGCAGGGCCTGCAATGTCAAGTCTGCAGCTTTGTGGTTCACCGCCGATGCCACGAATTTGTGA

250 260 270 280 290 300 310 320
CCTTCGAGTGTCCAGGCGCTGGAAGGGGCCCCAGACGGACGACCCTCGCAACAAGCACAAGTTCGGTCTGCACAGC
.....
CCTTCGAGTGTCCAGGCGCTGGAAGGGGCCCCAGACGGACGACCCTCGCAACAAGCACAAGTTCGGTCTGCACAGC

330 340 350 360 370 380 390
TACAGCAGTCCCACCTTCTGCGACCACTGTGGTTCCCTCCTCTACGGGCTGGTGCACCAGGGCATGAAATGTTCTTG
.....
TACAGCAGTCCCACCTTCTGCGACCACTGTGGTTCCCTCCTCTACGGGCTGGTGCACCAGGGCATGAAATGTTCTTG

400 410 420 430 440 450 460 470
TTGCGAAATGAATGTGCACCGACGCTGTGTGCGCAGCGTGCCCTCCCTTTGCGGCGTGGACCATAACAGAGCGCCGTG
.....
TTGCGAAATGAATGTGCACCGACGCTGTGTGCGCAGCGTGCCCTCCCTTTGCGGCGTGGACCATAACAGAGCGCCGTG

480 490 500 510 520 530 540 550
GACGTCTGCAACTGGAAATCCGGGCTCCACATCAGATGAGATCCATATTACTGTGGGTGAGGCCCGGAACCTCATT
.....
GACGTCTGCAACTGGAAATCCGGGCTCCACATCAGATGAGATCCATATTACTGTGGGTGAGGCCCGGAACCTCATT

560 570 580 590 600 610 620
CCTATGGACCCCAATGGCCTGTCTGATCCCTATGTGAACTGAAGCTCATCCCGGACCCTCGGAACCTGACAAAACA
.....
CCTATGGACCCCAATGGCCTGTCTGATCCCTATGTGAACTGAAGCTCATCCCGGACCCTCGGAACCTGACAAAACA

630 640 650 660 670 680 690 700
GAAGACAAAGACCGTGAAAGCCACACTGAATCCCGTGTGGAACGAGACCTTCGTGTTCAACCTGAAGCCGGGGGATG
.....
GAAGACAAAGACCGTGAAAGCCACACTGAATCCCGTGTGGAACGAGACCTTCGTGTTCAACCTGAAGCCGGGGGATG

13/26

FIGURE 7 (CONT)

710 720 730 740 750 760 770 780
TGGAGCGCCGGCTCAGTGTGGAGGTGTGGGATTGGGATAGGACATCCCGAAATGACTTCATGGGTGCCATGTCCTTT
.....
TGGAGCGCCGGCTCAGTGTGGAGGTGTGGGATTGGGATAGGACATCCCGAAATGACTTCATGGGTGCCATGTCCTTT
.....

790 800 810 820 830 840 850 860
GGTGTCTCAGAGCTACTCAAGGCTCCTGTGGATGGATGGTACAAGTTACTGAACCAGGAGGAGGGCGAGTATTACAA
.....
GGTGTCTCAGAGCTACTCAAGGCTCCTGTGGATGGATGGTACAAGTTACTGAACCAGGAGGAGGGCGAGTATTACAA
.....

870 880 890 900 910 920 930
TGTACCGGTGGCCGATGCTGACAAGTGCAGCCTCCTCCAGAAGTTTGAGGCCTGTAATTACCCCTTGGGAATTGTATG
.....
TGTACCGGTGGCCGATGCTGACAAGTGCAGCCTCCTCCAGAAGTTTGAGGCCTGTAATTACCCCTTGGGAATTGTATG
.....

940 950 960 970 980 990 1000 1010
AGAGAGTGGGATGGGCCCCCTCTTCTCTCCCATTCCTTCTCCATCCCCCAGTCCCGGACTCCAAGAGATGCTTC
.....
AGAGAGTGGGATGGGCCCCCTCTTCTCTCCCATTCCTTCTCCATCCCCCAGTCCCGGACTCCAAGAGATGCTTC
.....

1020 1030 1040 1050 1060 1070 1080 1090
TTCGGTGCCAGCCAGGACGCTGCATATCTCTGACTTCAGCTTCTCATGGTTCTAGGGAAAGGCAGTTTGGGAA
.....
TTCGGTGCCAGCCAGGACGCTGCATATCTCTGACTTCAGCTTCTCATGGTTCTAGGGAAAGGCAGTTTGGGAA
.....

1100 1110 1120 1130 1140 1150 1160
GGTGTATGCTGGCAGAGCGCAGAGGATCCGATGAACTCTATGCCATCAAGATACTGAAAAAGACGTCATTGTCCAGG
.....
GGTGTATGCTGGCAGAGCGCAGAGGATCCGATGAACTCTATGCCATCAAGATACTGAAAAAGACGTCATTGTCCAGG
.....

1170 1180 1190 1200 1210 1220 1230 1240
ATGATGATGTAGACTGCACCCCTTGTGGAGAAGCGTGTGCTGGCATTGGGAGGCCGAGGTCCTGGAGGCCGCCACAC
.....
ATGATGATGTAGACTGCACCCCTTGTGGAGAAGCGTGTGCTGGCATTGGGAGGCCGAGGTCCTGGAGGCCGCCACAC
.....

1250 1260 1270 1280 1290 1300 1310 1320
TTTCTCACACAACCTTCATTCCACCTTCAGACTCCGGACCGCCTGTATTTGTGATGGAGTACGTCACTGGGGGCGA
.....
TTTCTCACACAACCTTCATTCCACCTTCAGACTCCGGACCGCCTGTATTTGTGATGGAGTACGTCACTGGGGGCGA
.....

1330 1340 1350 1360 1370 1380 1390
TTTAATGTACCACATTGAGCAACTGGGCAAGTTTAAGGAGCCCCACGCAGCATTCTATGCCGCGGAAATCGCCATAG
.....
TTTAATGTACCACATTGAGCAACTGGGCAAGTTTAAGGAGCCCCACGCAGCATTCTATGCCGCGGAAATCGCCATAG
.....

1400 1410 1420 1430 1440 1450 1460 1470
GCCTCTTCTTCTTCAACAGGGCATCATCTACAGGGACCTCAAGTTGGATAATGTGATGCTGGATGCTGAAGGA
.....
GCCTCTTCTTCTTCAACAGGGCATCATCTACAGGGACCTCAAGTTGGATAATGTGATGCTGGATGCTGAAGGA
.....

1480 1490 1500 1510 1520 1530 1540 1550
CACATCAAGATCACAGACTTCGGCATGTGTAAAGAGAATGTCTTCCCTGGGTCCACAACCCGCACCTTCTGTGGGAC
.....
CACATCAAGATCACAGACTTCGGCATGTGTAAAGAGAATGTCTTCCCTGGGTCCACAACCCGCACCTTCTGTGGGAC
.....

14/26

FIGURE 7 (CONT)

1560 1570 1580 1590 1600 1610 1620 1630
CCCAGACTACATAGCACCTGAGATCATTGCCTATCAGCCCTATGGGAAGTCTGTCTGACTGGTGGTCCTTTGGAGTCC
.....
CCCAGACTACATAGCACCTGAGATCATTGCCTATCAGCCCTATGGGAAGTCTGTCTGACTGGTGGTCCTTTGGAGTCC

1640 1650 1660 1670 1680 1690 1700
TGCTGTATGAGATGTTGGCAGGACAGCCACCCTTTGATGGGGAAGATGAGGAGGAGCTGTTTCAAGCCATCATGGAA
.....
TGCTGTATGAGATGTTGGCAGGACAGCCACCCTTTGATGGGGAAGATGAGGAGGAGCTGTTTCAAGCCATCATGGAA

1710 1720 1730 1740 1750 1760 1770 1780
CAAACGTGCACCTATCCCAAGTCACCTTTCCCGGGAAGCTGTGGCCATCTGCAAGGGGTTCTTGACCAAGCACCCAGG
.....
CAAACGTGCACCTATCCCAAGTCACCTTTCCCGGGAAGCTGTGGCCATCTGCAAGGGGTTCTTGACCAAGCACCCAGG

1790 1800 1810 1820 1830 1840 1850 1860
AAAGCGCCTGGGCTCAGGGCCAGATGGGGAACCCACCATCCGGGCTCATGGCTTTTCCGTTGGATCGATTGGGAGA
.....
AAAGCGCCTGGGCTCAGGGCCAGATGGGGAACCCACCATCCGGGCTCATGGCTTTTCCGTTGGATCGATTGGGAGA

1870 1880 1890 1900 1910 1920 1930
GGTTGGAGAGACTGGAAATTGCGCCTCCTTTTAGACCACGTCCTGTGGCCGCGAGCGGCGAAAACCTTTGACAAGTTC
.....
GGTTGGAGAGACTGGAAATTGCGCCTCCTTTTAGACCACGTCCTGTGGCCGCGAGCGGCGAAAACCTTTGACAAGTTC

1940 1950 1960 1970 1980 1990 2000 2010
TTCACGCGGGCAGCGCCAGCCTTGACCCCGCCAGACCGCTTGGTCTAGCCAGCATCGACCAAGCTGATTTCAGGG
.....
TTCACGCGGGCAGCGCCAGCCTTGACCCCGCCAGACCGCTTGGTCTAGCCAGCATCGACCAAGCTGATTTCAGGG

2020 2030 2040 2050 2060 2070 2080 2090
CTTTACTTATGTGAACCCGGACTTCGTGCACCCAGATGCCCGCAGCCCCACAAGCCCTGTGCCCTGTGCCCGTCATG
.....
CTTTACTTATGTGAACCCGGACTTCGTGCACCCAGATGCCCGCAGCCCCACAAGCCCTGTGCCCTGTGCCCGTCATG

2100 2110 2120 2130 2140 2150 2160 2170
TAATCTCATCTGCTGCCGCTAGGTGTTCCAGTGCTCCCTCCGCCAAGTTGGCTGTAACCTCCCATCCACCCCATCCC
.....
TAATCTCATCTGCTGCCGCTAGGTGTTCCAGTGCTCCCTCCGCCAAGTTGGCTGTAACCTCCCATCCACCCCATCCC

Stop Codon

2180 2190 2200 2210 2220 2230 2240
CGCCTCTAGTCCGAATTTTAGGTCTCTTAAACCACCCAACCTTCTGGCCTCTTTACGCGCCCCAAGTGGGTTCTAG
.....
CGCCTCTAGTCCGAATTTTAGGTCTCTTAAACCACCCAACCTTCTGGCCTCTTTACGCGCCCCAA-TGGGTTCTAG

2250 2260 2270 2280 2290 2300 2310 2320
ACGCTGTTCCCGCAGCATTGCTGGCATTTTAAACTTCAAACAGTCTCTAGAGCCTTTCTGTGTTCTAGATTCGTTGTG
.....
ACGCTGTTCCCGCAGCATTGCTGGCATTTTAAACTTCAAACAGTCTCTAGAGCCTTTCTGTGTTCTAGATTCGTTGTG

15/26

FIGURE 7 (CONT)

```
      2330      2340      2350      2360      2370      2380      2390      2400
      |         |         |         |         |         |         |         |
CTGAGCCCTGGTTTTTCCCCACCCCCAACATCTGGATGCTGTTCCAACCTTTCCCAGAAACCCCACTCCGTGTGGGG
.....
CTGAGCCCTGGTTTTTCCCCACCCCCAACATCTGGATGCTGTTCCAACCTTTCCCAGAAACCCCACTCCGTGTGGGG

      2410      2420      2430      2440      2450      2460      2470
      |         |         |         |         |         |         |         |
TTCTAGACTCTATCTTGGTAGTTTTATGCCTTCTCTCTCCCTAGACCACGTTGGGAGAAATAGTCTCATGAGATTGC
.....
TTCTAGACTCTATCTTGGTAGTTTTATGCCTTCTCTCTCCCTAGACCACGTTGGGAGAAATAGTCTCATGAGATTGC

2480      2490      2500      2510      2520      2530      2540      2550
|         |         |         |         |         |         |         |
CTGCTCCAGACTAAGATTCCAGATCAGCTCTCTGCATCCTTCAAGGCCCTCCTACCTCCACTTCAGTTGTAGAA
.....
CTGCTCCAGACTAAGATTCCAGATCAGCTCTCTGCATCCTTCAAGGCCCTCCTACCTCCACTTCAGTTGTAGAA
```

16/26

FIGURE 8

M13977
Human clone 28
Z15114

-190 -180 -170 -160 -150 -140
CCTTGGCGAGCCGGCGCGCCCGGGGTGCCGCTCCCTGCCTGGCGCGCTCCGCACCTG

M13977
Human clone 28
Z15114

-130 -120 -110 -100 -90
GAGGTGCCTTGCCCTCTCCTGCCACCTCGGAATTTCCCTGTGGCTCCTTTGATCC
CCTTTGATCC

M13977
Human clone 28
Z15114

-80 -70 -60 -50 -40 -30
TTCGAGTCTCCAGCTCCTCTCCCTTCCACCTGTTTCCCCCAAGAAAGGCAGGATCCT
TTCGAGTCTCCAGCTCCTCTCCCTTCCACCTGTTTCCCCCAAGAAAGGCAGGATCCT

M13977
Human clone 28
Z15114

-20 -10 1 10 20 30
GGTCCCTGCTACGTTTCTGGGGCCATGGCTGGTCTGGGCCCCGGCGTAGGCGATTCA
GGTCCCTGCTACGTTTCTGGGGCCATGGCTGGTCTGGGCCCCGGCGTAGGCGATTCA

Start codon

M13977
Human clone 28
Z15114

40 50 60 70 80
GAGGGGGGACCCCGGCCCTGTTCTGCAGAAAGGGGGCTCTGAGGCAGAAGGTGGTC
GAGGGGGGACCCCGGCCCTGTTTTCAGAAAGGGGGCTCTGAGGCAGAAGGTGGTC

M13977
Human clone 28
Z15114

90 100 110 120 130 140
CACGAAGTCAAGAGCCACAAGTTACCGCTCGCTTCTTCAAGCAGCCACCTTCTGC
CACGAAGTCAAGAGCCACAAGTTACCGCTCGCTTCTTCAAGCAGCCACCTTCTGC

M13977
Human clone 28
Z15114

150 160 170 180 190 200
AGCCACTGCACCGACTTCATCTGGGGTATCGGAAAGCAGGGCCTGCAATGTCAAGTC
AGCCACTGCACCGACTTCATCTGGGGTATCGGAAAGCAGGGCCTGCAATGTCAAGTC

M13977
Human clone 28
Z15114

210 220 230 240 250 260
TGCAGCTTTGTGGTTTCATCGACGATGCCACGAATTTGTGACCTTCGAGTGTCCAGGC
TGCAGCTTTGTGGTTTCATCGACGATGCCACGAATTTGTGACCTTCGAGTGTCCAGGC

M13977
Human clone 28
Z15114

270 280 290 300 310
GCTGGGAAGGGCCCCCAGACGGACGACCCCGGAACAAACACAAGTTCCGCCTGCAT
GCTGGGAAGGGCCCCCAGACGGACGACCCCGGAACAAACACAAGTTCCGCCTGCAT

M13977
Human clone 28
Z15114

320 330 340 350 360 370
AGCTACAGCAGCCCCACCTTCTGCGACCACTGTGGCTCCCTCCTCTACGGGCTTGTG
AGCTACAGCAGCCCCACCTTCTGCGACCACTGTGGCTCCCTCCTCTACGGGCTTGTG

M13977
Human clone 28
Z15114

380 390 400 410 420 430
CACCAGGGCATGAAATGTTCTTGCTGCGAGATGAACGTGCACCGGCGCTGTGTGCG
CACCAGGGCATGAAATGCTCCTGCTGCGAGATGAACGTGCACCGGCGCTGTGTGCG

17/26

FIGURE 8 (CONT)

M13977
Human clone 28
Z15114

440 450 460 470 480
TAGCGTGCCCTCTCTGTGCGGTGTGGACCACACCGAGCGCCGCGGGCGCCTGCAGCT
TAGCGTGCCCTCCCTGTGCGGTGTGGACCACACCGAGCGCCGCGGGCGCCTGCAGCT
TGCAGCT

M13977
Human clone 28
Z15114

490 500 510 520 530 540
GGAGATCCGGGCTCCACAGCAGATGAGATCCACGTAACCTGTTGGCGAGGCCCGTAA
GGAGATCCGGGCTCCACAGCAGATGAGATCCACGTAACCTGTTGGCGAGGCCCGTAA
GGAGATCCGGGCTCCACAGCAGATGAGATCCACGTAACCTGTTGGCGAGGCCCGTAA

M13977
Human clone 28
Z15114

550 560 570 580 590 600
CCTAATTCCTATGGACCCCAATGGTCTCTCTGATCCCTATGTGAACTGAAGCTCAT
CCTAATTCCTATGGACCCCAACGGTCTCTCTGATCCCTATGTGAACTGAAGCTCAT
CCTAATTCCTATGGACCCCAATGGTCTCTCTGATCCCTATGTGAACTGAAGCTCAT

M13977
Human clone 28
Z15114

610 620 630 640 650
CCCAGACCTCGGAACCTGACGAAACAGAAGACCCGAACGGTGAAAGCCACGCTAAA
CCCAGACCTCGGAACCTGACGAAACAGAAGACCCGAACGGTGAAAGCCACGCTAAA
CCCAGACCTCGGAACCTGACGAAACAGAAGACCCGAACGGTGAAAGCCACGCTAAA

M13977
Human clone 28
Z15114

660 670 680 690 700 710
CCCTGTGTGGAATGAGACCTTTGTGTTCAACCTGAAGCCAGGGGATGTGGAGCGCCG
CCCTGTGTGGAATGAGACCTTTGTGTTCAACCTGAAGCCAGGGGATGTGGAGCGCCG
CCCTGTGTGGAATGAGACCTTTGTGTTCAACCTGAAGCCAGGGGATGTGGAGCGCCG

M13977
Human clone 28
Z15114

720 730 740 750 760 770
GCTCAGCGTGGAGGTGTGGGACTGGGACCGGACCTCCCGCAACGACTTCATGGGGGC
GCTCAGCGTGGAGGTGTGGGACTGGGACCGGACCTCCCGCAACGACTTCATGGGGGC
GCTCAGCGTGGAGGTGTGGGACTGGGACCGGACCTCCCGCAACGACTTCATGGGGGC

M13977
Human clone 28
Z15114

780 790 800 810 820 830
CATGTCCTTTGGCGTCTCGGAGCTGCTCAAGGCGCCCGTGGATGGCTGGTACAAGTT
CATGTCCTTTGGCGTCTCGGAGCTGCTCAAGGCGCCCGTGGATGGCTGGTACAAGTT
CATGTCCTTTGGCGTCTCGGAGCTGCTCAAGGCGCCCGTGGATGGCTGGTACAAGTT

M13977
Human clone 28
Z15114

840 850 860 870 880
ACTGAACCAGGAGGAGGGCGAGTATTACAATGTGCCGGTGGCTGATGCTGACAACCTG
ACTGAACCAGGAGGAGGGCGAGTATTACAATGTGCCGGTGGCCGATGCTGACAACCTG
ACTGAACCAGGAGGAGGGCGAGTATTACAATGTGCCGGTGGCCGATGCTGACAACCTG

M13977
Human clone 28
Z15114

890 900 910 920 930 940
CAGCCTCCTCCAGAAGTTTGAGGCTTGTAACCTACCCCTGGAATTGTATGA
CAGCCTCCTCCAGAAGTTTGAGGCTTGTAACCTACCCCTGGAATTGTATGAGCGGGT
CAGCCTCCTCCAGAAGTTTGAGGCTTGTAACCTACCCCTGGAATTGTATGAGCGGGT

M13977
Human clone 28
Z15114

950 960 970 980 990 1000
GCGGATGGGCCCCCTCTCTCTCCATCCCCCTCCCCCTTCCCTAGTCCCACCGACCC
GCGGATGGGCCCCCTCTCTCTCCATCCCCCTCCCCCTTCCCTAGTCCCACCGACCC

M13977
Human clone 28
Z15114

1010 1020 1030 1040 1050
CAAGCGCTGCTTCTTCGGGGCGAGTCCAGGACGCCTGCACATCTCCGACTTCAGCTT
CAAGCGCTGCTTCTTCGGGGCGAGTCCAGGACGCCTGCACATCTCCGACTTCAGCTT

18/26

FIGURE 8 (CONT)

M13977
Human clone 28
Z15114

1060 1070 1080 1090 1100 1110
| | | | | |
CCTCATGGTTCTAGGAAAAGGCAGTTTGGGAAGGTGATGCTGGCCGAGCGCAGGGG
CCTCATGGTTCTAGGAAAAGGCAGTTTGGGAAGGTGATGCTGGCCGAGCGCAGGGG

M13977
Human clone 28
Z15114

1120 1130 1140 1150 1160 1170
| | | | | |
CTCTGATGAGCTCTACGCCATCAAGATCTTGAAAAAGGACGTGATCGTCCAGGACGA
CTCTGATGAGCTCTACGCCATCAAGATCTTGAAAAAGGACGTGATCGTCCAGGACGA

M13977
Human clone 28
Z15114

1180 1190 1200 1210 1220
| | | | |
CGATGTGGACTGCACGCTGGTGGAGAAACGTGTGCTGGCGCTGGGGGGCCGGGGTCC
CGATGTGGACTGCACGCTGGTGGAGAAACGTGTGCTGGCGCTGGGGGGCCGGGGTCC

M13977
Human clone 28
Z15114

1230 1240 1250 1260 1270 1280
| | | | | |
TGGCGGGCCGGCCCCACTTCCTCACCCAGCTCCACTCCACCTTCCAGACCCCGGACC
TGGCGGGCCGGCCCCACTTCCTCACCCAGCTCCACTCCACCTTCCAGACCCCGGACC

M13977
Human clone 28
Z15114

1290 1300 1310 1320 1330 1340
| | | | | |
GCCTGTATTTTCGTGATGGAGTACGTCACCGGGGAGACTTGATGTACCACATTCAAC
GCCTGTATTTTCGTGATGGAGTACGTCACCGGGGAGACTTGATGTACCACATTCAAC

M13977
Human clone 28
Z15114

1350 1360 1370 1380 1390 1400
| | | | | |
AGCTGGGCAAGTTTAAGGAGCCCCATGCAGCGTTCTACGCGGCAGAAATCGCTATCG
AGCTGGGCAAGTTTAAGGAGCCCCATGCAGCGTTCTACGCGGCAGAAATCGCTATCG

M13977
Human clone 28
Z15114

1410 1420 1430 1440 1450
| | | | |
GCCTCTTCTTCCTTCACAATCAGGGCATCATCTACAGGGACCTGAAGCTGGACAATG
GCCTCTTCTTCCTTCACAATCAGGGCATCATCTACAGGGACCTGAAGCTGGACAATG

M13977
Human clone 28
Z15114

1460 1470 1480 1490 1500 1510
| | | | | |
TGATGCTGGATGCTGAGGGACACATCAAGATCACTGACTTTGGCATGTGTAAGGAGA
TGATGCTGGATGCTGAGGGACACATCAAGATCACTGACTTTGGCATGTGTAAGGAGA

M13977
Human clone 28
Z15114

1520 1530 1540 1550 1560 1570
| | | | | |
ACGTCTTCCCCGGGACGACAACCCGCACCTTCTGCGGGACCCCGGACTACATAGCCC
ACGTCTTCCCCGGGACGACAACCCGCACCTTCTGCGGGACCCCGGACTACATAGCCC

M13977
Human clone 28
Z15114

1580 1590 1600 1610 1620
| | | | |
CGGAGATCATTGCCTACCAGCCCTATGGGAAGTCTGTGCGATTGGTGGTCTTTGGAG
CGGAGATCATTGCCTACCAGCCCTATGGGAAGTCTGTGCGATTGGTGGTCTTTGGAG

M13977
Human clone 28
Z15114

1630 1640 1650 1660 1670 1680
| | | | | |
TTCTGCTGTATGAGATGTTGGCAGGACAGCCTCCCTTCGATGGGGAGGACGAGGAGG
TTCTGCTGTATGAGATGTTGGCAGGACAGCCTCCCTTCGATGGGGAGGACGAGGAGG

19/26

FIGURE 8 (CONT)

	1690	1700	1710	1720	1730	1740
M13977						
Human clone 28	AGCTGTTTCAGGCCATCATGGAACAACTGTCACCTACCCCAAGTCGCTTCCCCGGG					
Z15114	AGCTGTTTCAGGCCATCATGGAACAACTGTCACCTACCCCAAGTCGCTTCCCCGGG					
	1750	1760	1770	1780	1790	
M13977						
Human clone 28	AAGCCGTGGCCATCTGCAAGGGGTTCTTGACCAAGCACCCAGGGAAGCGCCTGGGCT					
Z15114	AAGCCGTGGCCATCTGCAAGGGGTTCTTGACCAAGCACCCAGGGAAGCGCCTGGGCT					
	1800	1810	1820	1830	1840	1850
M13977						
Human clone 28	CAGGGCCTGATGGGGAACCTACCATCCGTGCACATGGCTTTTTCCGCTGGATTGACT					
Z15114	CAGGGCCTGATGGGGAACCTACCATCCGTGCACATGGCTTTTTCCGCTGGATTGACT					
	1860	1870	1890	1900	2000	2010
M13977						
Human clone 28	GGGAGCGGCTGGAACGATTGGAGATCCCGCCTCCTTTTCAGACCCCGCCCGTGTGGCC					
Z15114	GGGAGCGGCTGGAACGATTGGAGATCCCGCCTCCTTTTCAGACCCCGCCCGTGTGGCC					
	2020	2030	2040	2050	2060	2070
M13977						
Human clone 28	GCAGCGGCGAGAACTTTGACAAGTTCTTCACGCGGGCGGCGCCAGCGCTGACCCCTC					
Z15114	GCAGCGGCGAGAACTTTGACAAGTTCTTCACGCGGGCGGCGCCAGCGCTGACCCCTC					
	2080	2090	2100	2110	2120	
M13977						
Human clone 28	CAGACCGCCTAGTCCTGGCCAGCATCGACCAGGCCGATTTCAGGGCTTCACCTACG					
Z15114	CAGACCGCCTAGTCCTGGCCAGCATCGACCAGGCCGATTTCAGGGCTTCACCTACG					
	2130	2140	2150	2160	2170	2180
M13977						
Human clone 28	TGAACCCGACTTCGTGCACCCGGATGCCCGCAGCCCCACCAGCCCAGTGCCTGTGC					
Z15114	TGAACCCGACTTCGTGCACCCGGATGCCCGCAGCCCCACCAGCCCAGTGCCTGTGC					
	2190	2200	2210	2220	2230	2240
M13977						
Human clone 28	CCGTCATGTAATCTCAC					
Z15114	CCGTCATGTAATCTCACCCGCGCCACTAGGTGTCCCCAACGTCCCCTCCGCCGTGC					
	Stop codon					
	2250	2260	2270	2280	2290	
M13977						
Human clone 28	CGGCGGCAGCCCCACTTCACCCCAACTTCACCACCCCTGTCCCATTCTAGATCCT					
Z15114	CGGCGGCAGCCCCACTTCACCCCAACTTCACCACCCCTGTCCCATTCTAGATCCT					
	2300	2310	2320	2330	2340	2350
M13977						
Human clone 28	GCACCCAGCATTCCAGCTCTGCCCCGCGGGTTCTAGACGCCCTCCCAAGCGTTC					
Z15114	GCACCCAGCATTCCAGCTCTGCCCCGCGGGTTCTAGACGCCCTCCCAAGCGTTC					
	2360	2370	2380	2390	2400	2410
M13977						
Human clone 28	CTGGCCTTCTGAACTCCATACAGCCTCTACAGCCGTCCCGCGTTCAAGACTTGAGCG					
Z15114	CTGGCCTTCTGAACTCCATACAGCCTCTACAGCCGTCCCGCGTTCAAGACTTGAGCG					

20/26

FIGURE 9

-140 -130 -120 -110 -100 -90 -80 -70
TGCTTTCTGCCCTGCGCTGCGCACCGTTAGTGCCCTGCCCTGTCTTCCGATCTCAGAGTCTGCGGAGTGCCCCCTA
.....
CCTTCCGATCTCAGAGTCTGCGGAGTGCCCCCTA

-60 -50 -40 -30 -20 -10 1 10
TCGCCGTCCACCTGTTTCTCAGAAAAAGGCCAGCTCGTGATCCCTGCTGCGTTCCTGGGGCCATGGCGGGTCTGG
.....
TCGCCGTCCACCTGTTTCTCAGAAAAAGGCCAGCTCGTGATCCCTGCTGCGTTCCTGGGGCCATGGCGGGTCTGG
Start Codon

20 30 40 50 60 70 80
GTCCTGGCGGGGGCGACTCAGAAGGGGGACCCCGACCCCTGTTTGCAGAAAGGGGGCGCTGAGGCAGAAGGTGGTC
.....
GTCCTGGCGGGGGCGACTCAGAAGGGGGACCCCGACCCCTGTTTGCAGAAAGGGGGCGCTGAGGCAGAAGGTGGTC

90 100 110 120 130 140 150 160
CACGAGGTGAAGAGCCACAAGTTCACCGCTCGTTTCTTCAAGCAGCCAACCTTCTGCAGTCACTGTACCGACTTCAT
.....
CACGAGGTGAAGAGCCACAAGTTCACCGCTCGTTTCTTCAAGCAGCCAACCTTCTGCAGTCACTGTACCGACTTCAT

170 180 190 200 210 220 230 240
CTGGGGCATTGGAAGCAGGGCCTGCAATGTCAAGTCTGCAGCTTTGTGGTTACCGCCGATGCCACGAATTTGTGA
.....
CTGGGGCATTGGAAGCAGGGCCTGCAATGTCAAGTCTGCAGCTTTGTGGTTACCGCCGATGCCACGAATTTGTGA

250 260 270 280 290 300 310 320
CCTTCGAGTGTCCAGGCGCTGGAAAGGGCCCCCAGACGGACGACCTCGCAACAAGCACAAGTTCGGTCTGCACAGC
.....
CCTTCGAGTGTCCAGGCGCTGGAAAGGGCCCCCAGACGGACGACCTCGCAACAAGCACAAGTTCGGTCTGCACAGC

330 340 350 360 370 380 390
TACAGCAGTCCCACCTTCTGCGACCACTGTGGTTCCCTCCTCTACGGGCTGGTGACCAAGGGCATGAAATGTTCTCTG
.....
TACAGCAGTCCCACCTTCTGCGACCACTGTGGTTCCCTCCTCTACGGGCTGGTGACCAAGGGCATGAAATGTTCTCTG

400 410 420 430 440 450 460 470
TTGCGAAATGAATGTGCACCGACGCTGTGTGCGCAGCGTGCCCTCCCTTTGCGGGCTGGACCATAACAGAGCGCCGTG
.....
TTGCGAAATGAATGTGCACCGACGCTGTGTGCGCAGCGTGCCCTCCCTTTGCGGGCTGGACCATAACAGAGCGCCGTG

480 490 500 510 520 530 540 550
GACGTCTGCAACTGGAAATCCGGGCTCCACATCAGATGAGATCCATATTACTGTGGGTGAGGCCCGGAACCTCATT
.....
GACGTCTGCAACTGGAAATCCGGGCTCCACATCAGATGAGATCCATATTACTGTGGGTGAGGCCCGGAACCTCATT

21/26

FIGURE 9 (CONT)

560 570 580 590 600 610 620
CCTATGGACCCCAATGGCCTGTCTGATCCCTATGTGAACTGAAGCTCATCCCGGACCCTCGGAACCTGACAAAACA
.....
CCTATGGACCCCAATGGCCTGTCTGATCCCTATGTGAACTGAAGCTCATCCCGGACCCTCGGAACCTGACAAAACA

630 640 650 660 670 680 690 700
GAAGACAAAGACCGTGAAAGCCACACTGAATCCCGTGTGGAACGAGACCTTCGTGTTCAACCTGAAGCCGGGGGATG
.....
GAAGACAAAGACCGTGAAAGCCACACTGAATCCCGTGTGGAACGAGACCTTCGTGTTCAACCTGAAGCCGGGGGATG

710 720 730 740 750 760 770 780
TGGAGCGCCGGCTCAGTGTGGAGGTGTGGGATTGGGATAGGACATCCCGAAATGACTTCATGGGTGCCATGTCCTTT
.....
TGGAGCGCCGGCTCAGTGTGGAGGTGTGGGATTGGGATAGGACATCCCGAAATGACTTCATGGGTGCCATGTCCTTT

790 800 810 820 830 840 850
GGTGTCTCAGAGCTACTCAAGGCTCCTGTGGATGGATGGTACAAGTTACTGAACCAGGAGGAGGGCGAGTATTACAA
.....
GGTGTCTCAGAGCTACTCAAGGCTCCTGTGGATGGATGGTACAAGTTACTGAACCAGTAGGAGGGCGAGTATTACAA
Stop Codon

860 870 880 890 900 910 920 930
TGTACCGGTGGCCGATGCTGACAACTGCAGCCTCCTCCAGAAGTTTGAGGCCTGTAATTACCCCTTGAATTGTATG
.....
TGTACCGGTGGCCGATGCTGACAACTGCAGCCTCCTCCAGAAGTTTGAGGCCTGTAATTACCCCTTGAATTGTATG

940 950 960 970 980 990 1000 1010
AGAGAGTGCGGATGGGCCCCCTCTCCTCTCCCATTCCTTCTCCATCCCCAGTCCACGGACTCCAAGAGATGCTTC
.....
AGAGAGTGCGGATGGGCCCCCTCTCCTCTCCCATTCCTTCTCCATCCCCAGTCCACGGACTCCAAGAGATGCTTC

1020 1030 1040 1050 1060 1070 1080
TTCGGTGCCAGCCCAGGACGCCTGCATATCTCTGACTTCAGCTTCCTCATGGTTCTAGGGAAAGGCAGTTTGGGAA
.....
TTCGGTGCCAGCCCAGGACGCCTGCATATCTCTGACTTCAGCTTCCTCATGGTTCTAGGGAAAGGCAGTTTGGGAA

1090 1100 1110 1120 1130 1140 1150 1160
GGTGATGCTGGCAGAGCGCAGAGGATCCGATGAACTCTATGCCATCAAGATACTGAAAAAAGACGTCATTGTCCAGG
.....
GGTGATGCTGGCAGAGCGCAGAGGATCCGATGAACTCTATGCCATCAAGATACTGAAAAAAGACGTCATTGTCCAGG

1170 1180 1190 1200 1210 1220 1230 1240
ATGATGATGTAGACTGCACCCTTGTGGAGAAGCGTGTGCTGGCATTGGGAGGCCGAGGTCCTGGAGGCCGGCCACAC
.....
ATGATGATGTAGACTGCACCCTTGTGGAGAAGCGTGTGCTGGCATTGGGAGGCCGAGGTCCTGGAGGCCGGCCACAC

22/26

FIGURE 9 (CONT)

1250 1260 1270 1280 1290 1300 1310 1320
TTTCTCACACAACCTTCATTCCACCTTTTCAGACTCCGGACCGCCTGTATTTTGTGATGGAGTACGTCACTGGGGGCGA
.....
TTTCTCACACAACCTTCATTCCACCTTTTCAGACTCCGGGCGCCTGTATTTTGTGATGGAGTACGTCACTGGGGGCGA

1330 1340 1350 1360 1370 1380 1390
TTTAATGTACCACATTTCAGCAACTGGGCAAGTTTAAGGAGCCCCACGCAGCATTCTATGCCGCGGAAATCGCCATAG
.....
TTTAATGTACCACATTTCAGCAACTGGGCAAGTTTAAGGAGCCCCACGCAGCATTCTATGCCGCGGAAATCGCCATAG

1400 1410 1420 1430 1440 1450 1460 1470
GCCTCTTCTTCTTCCTTCACAACCAGGGCATCATCTACAGGGACCTCAAGTTGGATAATGTGATGCTGGATGCTGAAGGA
.....
GCCTCTTCTTCTTCCTTCACAACCAGGGCATCATCTACAGGGACCTCAAGTTGGATAATGTGATGCTGGATGCTGAAGGA

1480 1490 1500 1510 1520 1530 1540 1550
CACATCAAGATCACAGACTTCGGCATGTGTAAAGAGAATGTCTTCCCTGGGTCCACAACCCGCACCTTCTGTGGGAC
.....
CACATCAAGATCACAGACTTCGGCATGTGTAAAGAGAATGTCTTCCCTGGGTCCACAACCCGCACCTTCTGTGGGAC

1560 1570 1580 1590 1600 1610 1620
CCCAGACTACATAGCACCTGAGATCATTGCCTATCAGCCCTATGGGAAGTCTGTGCGACTGGTGGTCTTTGGAGTCC
.....
CCCAGACTACATAGCACCTGAGATCATTGCCTATCAGCCCTATGGGAAGTCTGTGCGACTGGTGGTCTTTGGAGTCC

1630 1640 1650 1660 1670 1680 1690 1700
TGCTGTATGAGATGTTGGCAGGACAGCCACCCTTTGATGGGGAAGATGAGGAGGAGCTGTTTCAAGCCATCATGGAA
.....
TGCTGTATGAGATGTTGGCAGGACAGCCACCCTTTGATGGGGAAGATGAGGAGGAGCTGTTTCAAGCCATCATGGAA

1710 1720 1730 1740 1750 1760 1770 1780
CAAAGTGTACCTATCCCAAGTCACTTTCCCGGGAAGCTGTGGCCATCTGCAAGGGGTTCTTGACCAAGCACCCAGG
.....
CAAAGTGTACCTATCCCAAGTCACTTTCCCGGGAAGCTGTGGCCATCTGCAAGGGGTTCTTGACCAAGCACCCAGG

1790 1800 1810 1820 1830 1840 1850
AAAGCGCCTGGGCTCAGGGCCAGATGGGGAACCCACCATCCGGGCTCATGGCTTTTTCCGTTGGATCGATTGGGAGA
.....
AAAGCGCCTGGGCTCAGGGCCAGATGGGGAACCCACCATCCGGGCTCATGGCTTTTTCCGTTGGATCGATTGGGAGA

1860 1870 1880 1890 1900 1910 1920 1930
GGTTGGAGAGACTGGAAATTGCGCCTCCTTTTAGACCACGTCCGTGTGGCCGCGAGCGGCGAAAACCTTGACAAGTTC
.....
GGTTGGAGAGACTGGAAATTGCGCCTCCTTTTAGACCACGTCCGTGTGGCCGCGAGCGGCGAAAACCTTGACAAGTTC

23/26

FIGURE 9 (CONT)

1940 1950 1960 1970 1980 1990 2000 2010
TTCACGCGGGCAGCGCCAGCCTTGACCCCGCCAGACCGCTTGGTCCTAGCCAGCATCGACCAAGCTGATTTCAGGG
.....
TTCACGCGGGCAGCGCCAGCCTTGACCCCGCCAGACCGCTTGGTCCTAGCCAGCATCGACCAAGCTGATTTCAGGG

2020 2030 2040 2050 2060 2070 2080
CTTTACTTATGTGAACCCGGACTTCGTGCACCCAGATGCCCGCAGCCCCACAAGCCCTGTGCCTGTGCCCGTCATG
.....
CTTTACTTATGTGAACCCGGACTTCGTGCACCCAGATGCCCGCAGCCCCACAAGCCCTGTGCCTGTGCCCGTCATG

2090 2100 2110 2120 2130 2140 2150 2160
TAATCTCATCTGCTGCCGCTAGGTGTTCCCAAGTGCTCCCTCCGCCAAGTTGGCTGTAACCTCCCATCCACCCCATCC
.....
TAATCTCATCTGCTGCCGCTAGGTGTTCCCAAGTGCTC
Stop Codon

2170 2180 2190 2200 2210 2220 2230 2240
CGCCTCTAGTCCGAATTTTAGGTCTCTTAAACCACCCCAACCTTCTGGCCTCTTTCACGCGCCCCAAGTGGGTCTAG

2250 2260 2270 2280 2290 2300 2310 2320
ACGCTGTTCCCCAGCATTGCTGGCATTTTAACTTCAAACAGTCTCTAGAGCCTTCTGTGTTCTAGATTGTTGTG

2330 2340 2350 2360 2370 2380 2390
CTGAGCCCTGGTTTTTCCCCACCCCAACATCTGGATGCTGTTCCAACCTTCTCCAGAAACCCCACTCCGTGTGGGG

2400 2410 2420 2430 2440 2450 2460 2470
TTCTAGACTCTATCTTGGTAGTTTTATGCCTTCTCTCTCCCTAGACCACGTTGGGAGAAATAGTCTCATGAGATTGC

2480 2490 2500 2510 2520 2530 2540 2550
CTGCTCCAGACTAAGATTCCAGATCAGCTCTCTGCATCCTTCAAGGCCCTCTACCTCCACTTCAGTTGTAGAATT

2560 2570 2580 2590 2600 2610 2620
AAGTGGGAGGCTGGGCTCCGTGTTCCAGGCCACCTCCCTTCCATGTTCTGGGGATTCTGGCATGCACGGAGGATTC

2630 2640 2650 2660 2670 2680 2690 2700
TCTCCCCGACTTTTCTCAGTCAGCTTTTGTCTAGATTGTTCCAGAACCCTTCACTGCTCACCTGCCCCGTGCATG

2710 2720 2730 2740 2750 2760 2770 2780
GCTCCAGCCTTGGTCGGAATCACCCCT

2790 2800 2810 2820 2830 2840 2850
TGTCTCCGCAGTGCCCTGCACTTTCTGGGACTTTCTCATCCCCACGCCCTTCCTTTATCCTCTCCACCCAGACA

2860 2870 2880
CAGCTGCTGGAGAATAAATTG

24/26

FIGURE 10

10 20 30 40 50 60 70
MAGLGPGGGDSEGGPRPLFCRKALRQKVVEVKSHKFTARFFKQPTFCSHCTDFIWGIGKQGLQCQVCSFVVHRRC
.....
MAGLGPGGGDSEGGPRPLFCRKALRQKVVEVKSHKFTARFFKQPTFCSHCTDFIWGIGKQGLQCQVCSFVVHRRC

80 90 100 110 120 130 140 150
HEFVTFECPGAGKGPQTDDPRNKHKFRLLHSYSSPTFCDHCGSLLYGLVHQGMKSCCEMNVHRRCVRSVPSLCGVDH
.....
HEFVTFECPGAGKGPQTDDPRNKHKFRLLHSYSSPTFCDHCGSLLYGLVHQGMKSCCEMNVHRRCVRSVPSLCGVDH

160 170 180 190 200 210 220 230
TERRGRLQLEIRAPTSDEIHITVGEARNLIPMDPNGLSDPYVKLKLIPDPRNLTKQKTKTVKATLNPVWNETFVFNL
.....
TERRGRLQLEIRAPTSDEIHITVGEARNLIPMDPNGLSDPYVKLKLIPDPRNLTKQKTKTVKATLNPVWNETFVFNL

240 250 260 270 280
KPGDVERRLSVEVWDWDRTSRNDFMGAMSGVSELLKAPVDGWYKLLNQ
.....
KPGDVERRLSVEVWDWDRTSRNDFMGAMSGVSELLKAPVDGWYKLLNQEEGEYYNVPVADADNCSLLQKFEACNYP

LELYERVRMGPPSSSPIPSPSPSPTDSKRCFFGASPGRLHISDFSLMVLGKGSFGKVMLAERRGSDELYAIKILKDD

310 320 330 340 350 360 370 380
VIVQDDDDVDCTLVEKRVLALGGRGPGGRPHFLTQLHSTFQTPDRLYFVMEYVTGGDLMYHIQQLGKFKEPHAAFYAA

390 400 410 420 430 440 450 460
EIAIGLFFLHNQGI IYRDLKLDNVMMLDAEGHIKITDFGMCKENVFPGSTTRTFCTPDYIAPEIIAYQPYGKSVDWW

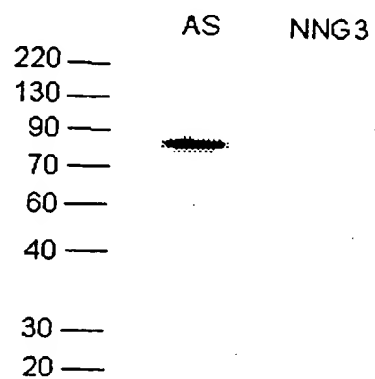
470 480 490 500 510 520 530
SFGVLLYEMLAGQPPFDGEDEEELFOAIMEQTVTPKSLSREAVAICKGFLTKHPGKRLGSGPDGEPTIRAHGFFRW

540 550 560 570 580 590 600 610
IDWERLERLEIAPPFRPRPCGRSGENFDKFFTRAAPALTPPDRILVLASIDQADFQGFYVNPDFVHPDARSPTSFPV

620 630 640 650 660 670 680 690

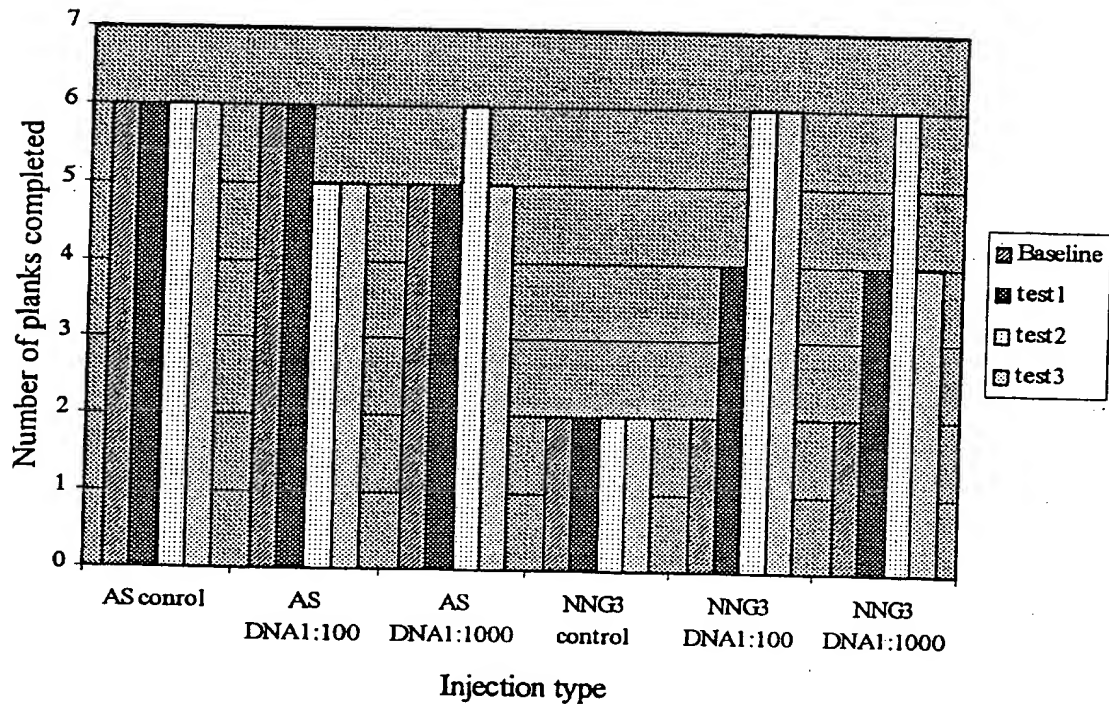
VPVM

25/26

FIGURE 11

26/26

FIGURE 12
Inclined Ramp Test - experiment 1



Inclined Ramp Test - experiment 2

